

19	34.8	5.7	624	10	US-10-301-480-335191	Sequence 335191,
20	34.8	5.7	624	10	US-10-301-480-948600,	Sequence 948600,
21	34.8	5.7	625	6	US-09-925-065A-256474	Sequence 256474,
22	34.2	5.6	191684	14	US-11-121-086-2	Sequence 2, Appli
23	33.6	5.5	681	8	US-10-750-185-63747	Sequence 63747, A
24	33.6	5.5	681	8	US-10-750-623-63747	Sequence 63747, A
25	33.4	5.4	6436	14	US-09-925-065A-544994	Sequence 544994, A
26	33.4	5.4	4236	14	US-11-122-329-117	Sequence 117, App
27	33	5.4	624	6	US-09-925-065A-544993	Sequence 544993,
28	33	5.4	825	6	US-09-925-065A-37189	Sequence 37189, A
29	33	5.4	825	9	US-10-301-480-138427	Sequence 138427,
30	33	5.4	825	10	US-10-301-480-751836	Sequence 751836,
31	33	5.4	1094	9	US-10-301-480-90687	Sequence 90687, A
32	33	5.4	1094	10	US-10-301-480-704096	Sequence 704096,
33	33	5.4	1610	6	US-09-925-065A-92085	Sequence 92085, A
34	33	5.4	1610	6	US-09-925-065A-92086	Sequence 92086, A
35	33	5.4	1610	6	US-09-925-065A-92087	Sequence 92087, A
36	33	5.4	1610	6	US-10-301-480-193327	Sequence 193327,
37	33	5.4	1610	9	US-10-301-480-193328	Sequence 193328,
38	33	5.4	1610	9	US-10-301-480-193329	Sequence 193329,
39	33	5.4	1610	10	US-10-301-480-806736	Sequence 806736,
40	33	5.4	1610	10	US-10-301-480-806737	Sequence 806737,
41	33	5.4	1610	10	US-10-301-480-806738	Sequence 806738,
42	32.6	5.3	14331	6	US-09-925-065A-717464	Sequence 717464,
43	32.4	5.3	655	6	US-09-925-065A-845210	Sequence 845210,
44	32.4	5.3	14082	8	US-10-995-561-13445	Sequence 13445, A
45	32.4	5.3	305312	8	US-10-995-561-13236	Sequence 13236, A

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RESULT 1
US-11-005-216-3
; Sequence 3, Application US/11005216
; Publication No. US20050287633A1
; GENERAL INFORMATION:
; APPLICANT: McIntyre, Peter
; APPLICANT: James, Iain Fraser
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/11/005,216
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US/09/533,220
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 1.30

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Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	8.0	5155	14	US-11-005-216-3
2	49.4	8.0	3014	14	US-11-077-716-1
3	49.4	8.0	33592	11	US-11-249-873-1
4	49.4	8.0	33699	11	US-11-249-873-3
5	49.4	8.0	33988	11	US-11-249-873-14
6	49.4	8.0	34341	11	US-11-249-873-2
7	49.4	8.0	34448	11	US-11-249-873-4
8	49.4	8.0	34555	8	US-10-623-155-479
9	49.4	8.0	34737	11	US-11-249-873-15
10	49.4	8.0	35696	8	US-10-860-436-1
11	49.4	8.0	35724	11	US-11-249-873-13
12	49.4	8.0	35893	8	US-10-860-436-2
13	49.4	8.0	35935	14	US-11-127-832-4
14	49.4	8.0	35935	14	US-11-127-832-5
15	49.4	8.0	35937	14	US-11-127-832-3
16	49.4	8.0	36114	11	US-11-249-873-16
17	47.8	7.8	12545	9	US-10-948-344-2
18	35	5.7	12400	14	US-11-127-832-26

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:20:15 ; Search time 800.831 Seconds
(without alignments)
6340.158 Million cell updates/sec

Title: US-10-781-055A-36

Perfect score: 614

Sequence: 1 cggatcatgatgtctcgat.....ctctcagtcagcgatcaa 614

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	614	7	US-10-781-055-36
2	568	92.5	596	7	US-10-781-055-37
3	190	30.9	190	7	US-10-781-055-35
4	60	9.8	60	7	US-10-781-055-3
5	51	8.3	51	7	US-10-781-055-1
6	49.4	8.0	3788	3	US-09-392-462-1
7	49.4	8.0	3788	3	US-09-540-991-1
8	49.4	8.0	3788	6	US-10-291-041-1
9	49.4	8.0	3788	7	US-10-351-603-1
10	49.4	8.0	5155	5	US-10-128-853-3
11	49.4	8.0	5374	5	US-10-007-357-7
12	49.4	8.0	5462	5	US-10-007-357-6
13	49.4	8.0	7522	8	US-10-491-121-36
14	49.4	8.0	7711	7	US-10-359-120-49
15	49.4	8.0	7711	8	US-10-491-121-35
16	49.4	8.0	7789	7	US-10-359-120-45
17	49.4	8.0	7789	7	US-10-359-120-46
18	49.4	8.0	7792	7	US-10-359-120-48
19	49.4	8.0	7828	7	US-10-359-120-47
20	49.4	8.0	7867	7	US-10-359-120-42
21	49.4	8.0	7870	7	US-10-359-120-39
22	49.4	8.0	7870	7	US-10-359-120-43
23	49.4	8.0	7885	7	US-10-359-120-44

24	49.4	8.0	7906	7	US-10-359-120-40	Sequence 40, Appl
25	49.4	8.0	7909	7	US-10-359-120-41	Sequence 41, Appl
26	49.4	8.0	7948	7	US-10-359-120-36	Sequence 36, Appl
27	49.4	8.0	7963	7	US-10-359-120-37	Sequence 37, Appl
28	49.4	8.0	7966	7	US-10-359-120-38	Sequence 38, Appl
29	49.4	8.0	7987	7	US-10-359-120-35	Sequence 35, Appl
30	49.4	8.0	8131	8	US-10-491-121-12	Sequence 12, Appl
31	49.4	8.0	8146	8	US-10-491-121-20	Sequence 20, Appl
32	49.4	8.0	8199	8	US-10-491-121-29	Sequence 29, Appl
33	49.4	8.0	8221	8	US-10-491-121-27	Sequence 27, Appl
34	49.4	8.0	8238	3	US-09-482-682-50	Sequence 50, Appl
35	49.4	8.0	8256	8	US-10-491-121-32	Sequence 32, Appl
36	49.4	8.0	8338	8	US-10-491-121-26	Sequence 26, Appl
37	49.4	8.0	8439	8	US-10-491-121-28	Sequence 28, Appl
38	49.4	8.0	10783	8	US-10-491-121-25	Sequence 25, Appl
39	49.4	8.0	30365	7	US-10-384-136-4	Sequence 4, Appl
40	49.4	8.0	31183	7	US-10-431-598-19	Sequence 19, Appl
41	49.4	8.0	31183	8	US-10-825-282-4	Sequence 4, Appl
42	49.4	8.0	31672	7	US-10-384-136-3	Sequence 3, Appl
43	49.4	8.0	31880	7	US-10-427-717-507	Sequence 507, App
44	49.4	8.0	31976	8	US-10-766-307A-1	Sequence 1, Appl
45	49.4	8.0	31976	8	US-10-766-307A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-781-055-36
; Sequence 36, Application US/10781055
; Publication No. US20040171573A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN
; APPLICANT: QU, BAO-XI
; TITLE OF INVENTION: RATIONALLY DESIGNED AND CHEMICALLY SYNTHESIZED
; TITLE OF INVENTION: PROMOTER FOR GENETIC VACCINE AND GENE THERAPY
; FILE REFERENCE: UTSD:788US
; CURRENT APPLICATION NUMBER: US/10/781,055
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/448,166
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 614
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-781-055-36

Query Match 100.0%; Score 614; DB 7; Length 614;
Best Local Similarity 100.0%; Pred. No. 2.6e-194; Mismatches 0; Indels 0; Gaps 0;
Matches 614; Conservative 0

QY	1	CGGTACATCATGTTCTTCGATGCAATATACGTAAGGTCACAAATAGGTCACAGGTCAACCT 60
Db	1	CGGTACATCATGTTCTTCGATGCAATATACGTAAGGTCACAAATAGGTCACAGGTCAACCT 60
QY	61	CTCTCGGCTATCAATAAGAGTGTAGGACCGGAGAGGGGAAAAACAGAACAGACAGTG 120
Db	61	CTCTCGGCTATCAATAAGAGTGTAGGACCGGAGAGGGGAAAAACAGAACAGACAGTG 120
QY	121	CTGAGCTCAGCAGGCGAGTTGCCCTTTGAAAACGTTAACGTTACGTTACGTTGCGACTGC 180
Db	121	CTGAGCTCAGCAGGCGAGTTGCCCTTTGAAAACGTTAACGTTACGTTACGTTGCGACTGC 180
QY	181	AGCTGATTAAATTAATACAGCCAAAGCGCCCAAGCAAGCTTATATGCAAAATATGCAAAAT 240
Db	181	AGCTGATTAAATTAATACAGCCAAAGCGCCCAAGCAAGCTTATATGCAAAATATGCAAAAT 240
QY	241	GAGAACAGGGGGGGGGGGCGGACATCGGTTCAACGTTTCTGGTTTCAATTTCTTCTCTAT 300

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:03:35 ; Search time 164.026 Seconds
(without alignments)
6553.974 Million cell updates/sec

Title: US-10-781-055A-36

Perfect score: 614

Sequence: 1 cggatcatgatgtctcgat.....ctctcagtcagcgatcaa 614

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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- 2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/PCITUS COMB.seq.*
- 7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49.4	8.0	382	2	US-08-333-706-1
2	49.4	8.0	643	2	US-08-458-372-21
3	49.4	8.0	643	8	US-09-384-327-21
4	49.4	8.0	872	2	US-08-458-372-20
5	49.4	8.0	872	8	US-09-384-327-20
6	49.4	8.0	874	9	5506118-10
7	49.4	8.0	2898	3	US-09-051-696-7
8	49.4	8.0	5155	3	US-09-533-220A-3
9	49.4	8.0	5155	3	US-10-128-853-3
10	49.4	8.0	5374	3	US-10-007-357-7
11	49.4	8.0	5462	3	US-10-007-357-6
12	49.4	8.0	6151	6	PCT-US91-02954-12
13	49.4	8.0	6306	6	PCT-US94-00658-1
14	49.4	8.0	32166	3	US-09-562-930-11
15	49.4	8.0	32798	3	US-09-604-6948-1
16	49.4	8.0	34303	2	US-08-735-609-4
17	49.4	8.0	34303	2	US-08-735-609-4
18	49.4	8.0	34303	3	US-09-315-372-4
19	49.4	8.0	34303	3	US-09-244-752-4
20	49.4	8.0	34303	3	US-09-245-497-4
21	49.4	8.0	34303	3	US-09-562-919-4
22	49.4	8.0	34382	2	US-08-374-483-6
23	49.4	8.0	3427	3	US-09-111-911-5
24	49.4	8.0	35408	3	US-08-973-334-3

25 49.4 8.0 35408 3 US-09-563-869A-3 Sequence 3, Appli
26 49.4 8.0 35408 3 US-08-549-489-3 Sequence 3, Appli
27 49.4 8.0 35871 3 US-09-956-335-2 Sequence 2, Appli
28 49.4 8.0 35935 2 US-08-735-609-1 Sequence 1, Appli
29 49.4 8.0 35935 2 US-08-735-609-1 Sequence 1, Appli
30 49.4 8.0 35935 3 US-08-379-452-43 Sequence 43, Appli
31 49.4 8.0 35935 3 US-09-315-372-1 Sequence 1, Appli
32 49.4 8.0 35935 3 US-09-244-752-1 Sequence 1, Appli
33 49.4 8.0 35935 3 US-09-245-497-1 Sequence 1, Appli
34 49.4 8.0 35935 3 US-09-409-670-43 Sequence 43, Appli
35 49.4 8.0 35935 3 US-09-562-919-1 Sequence 1, Appli
36 49.4 8.0 35935 3 US-09-782-378A-4 Sequence 4, Appli
37 49.4 8.0 35935 3 US-09-782-378A-5 Sequence 5, Appli
38 49.4 8.0 35937 3 US-09-956-335-1 Sequence 3, Appli
39 49.4 8.0 36620 3 US-09-952-060-25 Sequence 1, Appli
40 49.4 8.0 37474 3 US-09-952-060-25 Sequence 25, Appli
41 49.4 8.0 38519 3 US-09-952-060-28 Sequence 28, Appli
42 49.4 7.8 12445 3 US-09-865-022-2 Sequence 2, Appli
43 47.8 6.8 50 2 US-08-171-389-579 Sequence 579, App
44 42 6.8 50 2 US-08-171-389-580 Sequence 580, App
45 42 6.8 50 2

ALIGNMENTS

RESULT 1
US-08-333-706-1
; Sequence 1, Application US/08333706
; Patent No. 5612213
; GENERAL INFORMATION:
; APPLICANT: Chan, Sham-Yuen
; TITLE OF INVENTION: Vector and Mammalian Cell Line Having Improved
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: Fourth and Parker Streets
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,706
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/075,209
; FILING DATE: 10-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: CL-208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)420-5511
; TELEFAX: (510)428-4703
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-333-706-1

Query Match 8.0%; Score 49.4; DB 2; Length 382;
Best Local Similarity 89.6%; Pred. No. 5.2e-06;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:52:47 ; Search time 3978.28 Seconds
(without alignments)
7221.025 Million cell updates/sec

Title: US-10-781-055A-36
Perfect score: 614
Sequence: 1 cggatcatgatgtttctcat.....ctctcagtcctcagcgatcaa 614

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: qb est1:*
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CNSU16BE	CNS016BE	1201 bp	DNA linear	GSS 26-JUL-1999
LOCUS				
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC BACN15E23 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.			

ACCESSION	U010532	
VERSION	U010532.1	GI:5622404
KEYWORDS	GSS.	
SOURCE	<i>Drosophila melanogaster</i>	(fruit fly)
ORGANISM	<i>Drosophila melanogaster</i>	
	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 1201)	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Query			DB	ID	Description
		Score	Match	Length			
	1	39.6	6.4	1201	10	CNS016BE	AL106532 Drosophil
	2	38.2	6.2	1068	3	BM921844	BN921844 AGENCOURT
C	3	38	6.1	409	1	AI1857142	AI1857142 MENAad-A1
C	4	37.8	6.2	1064	9	B2427726	B2427726 CH230-457
5	5	37.6	6.1	590	10	CZ481855	CZ481855 e04097-5p
C	6	37.6	6.1	859	10	CNS0004Y	AL055406 Drosophil
	7	37.4	6.1	796	7	CR412210	CR412210 CR412210
C	8	37.2	6.1	1079	9	C230752	C230752 CH261-114
	9	36.8	6.0	568	6	CD125835	CD125835 MF1-0001U
	10	36.8	6.0	827	9	B2567513	B2567513 pac82-164
	11	36.8	6.0	984	10	CZ386907	CZ386907 ZMMBF0163
C	12	36.6	6.0	736	10	AG372972	AG372972 Mus muscu
C	13	36.6	6.0	757	11	CR806759	CR806759 GLOAA28D
	14	36.6	6.0	794	8	DN112025	DN112025 M111185 M
C	15	36.4	5.9	499	9	B2156401	B2156401 CH230-347
C	16	36.4	5.9	549	10	CZ433879	CZ433879 OA BBA009
17	17	36.4	5.9	1200	6	CD503874	CD503874 CDA64-G08
C	18	36.2	5.9	817	10	CZ998292	CZ998292 187615 To
C	19	36.2	5.9	914	1	AL544144	AL544144 AL544144
	20	36	5.9	612	9	BH679464	BH679464 BOHW433TF
21	21	36	5.9	737	8	DR339051	DR339051 TKN096H1
C	22	36	5.9	924	10	CL297903	CL297903 ZMMBB008

ORIGIN

Query Match 6.4%; Score 39.6; DB 10; Length 1201;
Best Local Similarity 28.5%; Pred. No. 1.5;
Matches 72; Conservative 69; Mismatches 112; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:41:05 ; Search time 556.547 Seconds
(without alignments)
7352.695 Million cell updates/sec

Title: US-10-781-055A-36
Perfect score: 614
Sequence: 1 cgtacatgatgtctcgat.....ctctcagtcacgcatgcaa 614

Scoring table: IDENTITY NUC
Gapox 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	614	13 ADR90243	Adr90243 SP72 prom
2	568	92.5	596	13 ADR90244	Adr90244 SP72 prom
3	190	30.9	190	13 ADR90242	Adr90242 SP72 prom
4	60	9.8	60	13 ADR90218	Adr90218 CREB/ATF
5	51	8.3	51	13 ADR90216	Adr90216 Vitamin D
6	49.4	8.0	382	2 AAT79748	Aat79748 AML promo
7	49.4	8.0	382	2 AAT60502	Aat60502 Adeno maj
8	49.4	8.0	382	1 AAV62387	Aav62387 Nucleotid
9	49.4	8.0	561	1 AAN50287	Aan50287 Sequence
10	49.4	8.0	578	1 AAN50288	Aan50288 Sequence
11	49.4	8.0	642	2 AAQ54210	Aaq54210 BK enhanc
12	49.4	8.0	642	2 AAQ58456	Aaq58456 BK enhanc
13	49.4	8.0	642	2 AAT15956	Aat15956 BK enhanc
14	49.4	8.0	643	2 AAT95172	Aat95172 Sequence
15	49.4	8.0	824	1 AAN70083	Aan70083 Sequence
16	49.4	8.0	848	2 AAQ13632	Aaq13632 GMT mod
17	49.4	8.0	873	3 AAQ39104	Aaq39104 Plasmid p
18	49.4	8.0	874	1 AAN70082	Aan70082 Sequence
19	49.4	8.0	874	2 AAQ03825	Aaq03825 Improved

20	49.4	8.0	874	2	AAQ54209	Aaq54209 BK enhanc
21	49.4	8.0	874	2	AAQ58455	Aaq58455 BK enhanc
22	49.4	8.0	874	2	AAT36645	Aat36645 BK enhanc
23	49.4	8.0	874	2	AAT15955	Aat15955 BK enhanc
24	49.4	8.0	874	2	AAT43793	Aat43793 BK enhanc
25	49.4	8.0	874	2	AAT95171	Aat95171 BK enhanc
26	49.4	8.0	874	2	AAX18483	Aax18483 BK enhanc
27	49.4	8.0	874	5	AAH45120	Aah45120 BK protot
28	49.4	8.0	3788	3	AAZ93330	Aaz93330 PG2A-CAT
29	49.4	8.0	3788	5	AAD21318	Aad21318 CpG alter
30	49.4	8.0	5155	6	AAD42468	Aad42468 Human pla
31	49.4	8.0	5155	8	ACA61961	Aca61961 Mammalian
32	49.4	8.0	5365	1	AAN90646	Aan90646 Nucleotid
33	49.4	8.0	5374	3	AAC60706	Aac60706 Primers a
34	49.4	8.0	5413	1	AAN90649	Aan90649 Nucleotid
35	49.4	8.0	5462	3	AAC60707	Aac60707 Primers a
36	49.4	8.0	5518	1	AAN90647	Aan90647 Nucleotid
37	49.4	8.0	5566	1	AAN90648	Aan90648 Nucleotid
38	49.4	8.0	6149	1	AAN90645	Aan90645 Sequence
39	49.4	8.0	6151	1	AAN90644	Aan90644 Sequence
40	49.4	8.0	6151	1	AAQ05608	Aaq05608 Plasmid p
41	49.4	8.0	6151	2	AAQ03006	Aaq03006 Full leng
42	49.4	8.0	6165	2	AAQ20324	Aaq20324 Sol.rhesu
43	49.4	8.0	7316	2	AAQ04555	Aaq04555 Plasmid p
44	49.4	8.0	7377	2	AAQ05607	Aaq05607 Plasmid p
45	49.4	8.0	7377	2	AAQ03005	Aaq03005 Full leng

ALIGNMENTS

RESULT 1
ADR90243
ID ADR90243 standard; DNA; 614 BP.
XX
AC ADR90243;
XX
DT 18-NOV-2004 (first entry)
XX
DE SP72 promoter DNA #2.
XX
KW Promoter/enhancer; cancer; infectious disease; inflammatory disease;
KW tuberculosis; hepatitis B; HIV-1; influenza; malaria; cytostatic;
KW vaccine; gene therapy; SP72 promoter; ds.
XX
OS Unidentified.
XX
PN US2004171573-A1.
XX
PD 02-SEP-2004.
XX
PP 18-FEB-2004; 2004US-00781055.
XX
PR 18-FEB-2003; 2003US-0448166P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Johnston S, Qu B;
XX
DR WPI; 2004-634560/61.
XX
PT New nucleic acid segment comprises SP72 synthetic promoter/enhancer,
PT useful as a vaccine for genetic immunization or for gene therapy for
PT treating or preventing cancers, infectious diseases, or inflammatory
PT diseases.
XX
PS Claim 13; SEQ ID NO 36; 34pp; English.
XX
CC The present invention provides nucleic acid segments comprising a
CC synthetic promoter/enhancer or its complement. The invention is useful
CC for treating or preventing diseases or conditions including cancers,
CC infectious diseases and inflammatory diseases such as viral and parasitic
CC including tuberculosis, hepatitis B, HIV-1, influenza and malaria. The

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	49.4	26.0	5155	14	US-11-007-216-3	Sequence
2	49.4	26.0	33014	14	US-11-077-716-1	Sequence
3	49.4	26.0	33592	11	US-11-249-873-1	Sequence
4	49.4	26.0	33699	11	US-11-249-873-3	Sequence
5	49.4	26.0	33988	11	US-11-249-873-14	Sequence
6	49.4	26.0	34341	11	US-11-249-873-2	Sequence
7	49.4	26.0	34448	11	US-11-249-873-4	Sequence
8	49.4	26.0	34555	8	US-10-623-155-479	Sequence 4
9	49.4	26.0	34737	11	US-11-249-873-15	Sequence 1
10	49.4	26.0	35696	8	US-10-860-436-1	Sequence 1
11	49.4	26.0	35724	11	US-11-249-873-13	Sequence 2
12	49.4	26.0	35893	8	US-10-860-436-2	Sequence
13	49.4	26.0	35935	14	US-11-127-832-4	Sequence
14	49.4	26.0	35935	14	US-11-127-832-5	Sequence
15	49.4	26.0	35937	11	US-11-127-832-3	Sequence
16	49.4	26.0	36114	11	US-11-249-873-16	Sequence
17	47.8	25.2	12445	9	US-10-948-344-2	Sequence 2
18	35	18.4	35100	14	US-11-127-832-26	Sequence

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:20:15 ; Search time 247.814 Seconds
(without alignments)
6340.158 Million cell updates/sec

Title: US-10-781-055A-35

Perfect score: 190

Sequence: 1 aaatgacataggaaactga.....ctctcagtcctcagcgatcaa 190

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	100.0	190	7	US-10-781-055-35
2	190	100.0	596	7	US-10-781-055-37
3	190	100.0	614	7	US-10-781-055-36
4	49.4	26.0	3788	3	US-09-392-462-1
5	49.4	26.0	3788	3	US-09-540-991-1
6	49.4	26.0	3788	6	US-10-291-041-1
7	49.4	26.0	3788	7	US-10-351-603-1
8	49.4	26.0	5155	5	US-10-128-853-3
9	49.4	26.0	5374	5	US-10-007-357-7
10	49.4	26.0	5462	5	US-10-007-357-6
11	49.4	26.0	7522	8	US-10-491-121-36
12	49.4	26.0	7711	7	US-10-359-120-49
13	49.4	26.0	7711	8	US-10-491-121-35
14	49.4	26.0	7789	7	US-10-359-120-45
15	49.4	26.0	7789	7	US-10-359-120-48
16	49.4	26.0	7792	7	US-10-359-120-46
17	49.4	26.0	7828	7	US-10-359-120-47
18	49.4	26.0	7867	7	US-10-359-120-42
19	49.4	26.0	7870	7	US-10-359-120-39
20	49.4	26.0	7870	7	US-10-359-120-43
21	49.4	26.0	7885	7	US-10-359-120-44
22	49.4	26.0	7906	7	US-10-359-120-40
23	49.4	26.0	7909	7	US-10-359-120-41

24 49.4 26.0 7948 7 US-10-359-120-36 Sequence 36, Appl
25 49.4 26.0 7963 7 US-10-359-120-37 Sequence 37, Appl
26 49.4 26.0 7966 7 US-10-359-120-38 Sequence 38, Appl
27 49.4 26.0 7987 7 US-10-359-120-35 Sequence 35, Appl
28 49.4 26.0 8131 8 US-10-491-121-12 Sequence 12, Appl
29 49.4 26.0 8146 8 US-10-491-121-20 Sequence 20, Appl
30 49.4 26.0 8199 8 US-10-491-121-29 Sequence 29, Appl
31 49.4 26.0 8221 8 US-10-491-121-27 Sequence 27, Appl
32 49.4 26.0 8238 3 US-09-482-682-50 Sequence 20, Appl
33 49.4 26.0 8256 8 US-10-491-121-32 Sequence 50, Appl
34 49.4 26.0 8338 8 US-10-491-121-26 Sequence 32, Appl
35 49.4 26.0 8439 8 US-10-491-121-25 Sequence 26, Appl
36 49.4 26.0 10783 8 US-10-491-121-25 Sequence 28, Appl
37 49.4 26.0 30365 7 US-10-384-136-4 Sequence 25, Appl
38 49.4 26.0 31183 7 US-10-431-598-19 Sequence 4, Appl
39 49.4 26.0 31183 8 US-10-825-282-4 Sequence 19, Appl
40 49.4 26.0 31672 7 US-10-384-136-3 Sequence 4, Appl
41 49.4 26.0 31880 7 US-10-427-717-507 Sequence 3, Appl
42 49.4 26.0 31976 8 US-10-766-307A-1 Sequence 507, App
43 49.4 26.0 31976 8 US-10-766-307A-2 Sequence 1, Appl
44 49.4 26.0 32409 10 US-11-104-126-2 Sequence 2, Appl
45 49.4 26.0 32480 3 US-09-847-101B-23 Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-10-781-055-35
; Sequence 35, Application US/10781055
; Publication No. US20040171573A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN
; APPLICANT: QU, BAO-XI
; TITLE OF INVENTION: RATIONALLY DESIGNED AND CHEMICALLY SYNTHESIZED
; TITLE OF INVENTION: PROMOTER FOR GENETIC VACCINE AND GENE THERAPY
; FILE REFERENCE: UTSD:788US
; CURRENT APPLICATION NUMBER: US/10/781,055
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/448,166
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 190
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-781-055-35

Query Match 100.0%; Score 190; DB 7; Length 190;
Best Local Similarity 100.0%; Pred. No. 4.3e-54;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATGACATAGGAAACTGACTCACAAGGAGAGTGAAGTGGGACTTTCCAAAGGCG 60
Db 1 AAATGACATAGGAAACTGACTCACAAGGAGAGTGAAGTGGGACTTTCCAAAGGCG 60

Qy 61 GGCCAAATTGGGGGGGGCCCGGTCTTCTGTAAGGGCGCTATATAAGGGGGGGCGGG 120
Db 61 GGCCAAATTGGGGGGGGCCCGGTCTTCTGTAAGGGCGCTATATAAGGGGGGGCGGG 120

Qy 121 CGCGTTTCGTCTCTCATTTCTGGACCGCGTCCGCGCCCGGACGAGAGCTGAGCTCTCAGTCT 180
Db 121 CGCGTTTCGTCTCTCATTTCTGGACCGCGTCCGCGCCCGGACGAGAGCTGAGCTCTCAGTCT 180

Qy 181 CAGCGATCAA 190
Db 181 CAGCGATCAA 190

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:03:35 ; Search time 50.7571 Seconds
(without alignments)
6653.974 Million cell updates/sec

Title: US-10-781-055A-35
Perfect score: 190
Sequence: 1 aaatgaataggaactga.....ctctcagtcacgacgtcaa 190

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCBUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	26.0	382	2	US-08-333-706-1
2	49.4	26.0	643	2	US-08-458-372-21
3	49.4	26.0	643	8	US-09-384-327-21
4	49.4	26.0	872	2	US-08-458-372-20
5	49.4	26.0	872	8	US-09-384-327-20
6	49.4	26.0	874	9	US-06118-10
7	49.4	26.0	2898	3	US-09-051-696-7
8	49.4	26.0	5155	3	US-09-533-220A-3
9	49.4	26.0	5155	3	US-10-128-853-3
10	49.4	26.0	5374	3	US-10-007-357-7
11	49.4	26.0	5462	3	US-10-007-357-6
12	49.4	26.0	6151	6	PCT-US91-02954-12
13	49.4	26.0	6306	6	PCT-US94-00658-1
14	49.4	26.0	32166	3	US-09-562-930-11
15	49.4	26.0	32798	3	US-09-604-694B-1
16	49.4	26.0	34303	2	US-08-735-609-4
17	49.4	26.0	34303	2	US-08-735-609-4
18	49.4	26.0	34303	3	US-09-315-372-4
19	49.4	26.0	34303	3	US-09-244-752-4
20	49.4	26.0	34303	3	US-09-245-497-4
21	49.4	26.0	34303	3	US-09-562-919-4
22	49.4	26.0	34382	2	US-08-374-483-6
23	49.4	26.0	34427	3	US-09-111-911-5
24	49.4	26.0	35408	3	US-08-973-334-3

25	49.4	26.0	35408	3	US-09-563-869A-3	Sequence 3, Appli
26	49.4	26.0	35408	3	US-08-549-489-3	Sequence 3, Appli
27	49.4	26.0	35871	3	US-09-956-335-2	Sequence 2, Appli
28	49.4	26.0	35935	2	US-08-735-609-1	Sequence 1, Appli
29	49.4	26.0	35935	2	US-08-735-609-1	Sequence 1, Appli
30	49.4	26.0	35935	3	US-08-379-452-43	Sequence 43, Appli
31	49.4	26.0	35935	3	US-09-315-372-1	Sequence 1, Appli
32	49.4	26.0	35935	3	US-09-244-752-1	Sequence 1, Appli
33	49.4	26.0	35935	3	US-09-245-497-1	Sequence 1, Appli
34	49.4	26.0	35935	3	US-09-409-670-43	Sequence 43, Appli
35	49.4	26.0	35935	3	US-09-562-919-1	Sequence 1, Appli
36	49.4	26.0	35935	3	US-09-782-378A-4	Sequence 4, Appli
37	49.4	26.0	35935	3	US-09-782-378A-5	Sequence 5, Appli
38	49.4	26.0	35937	3	US-09-782-378A-3	Sequence 3, Appli
39	49.4	26.0	35978	3	US-09-956-335-1	Sequence 1, Appli
40	49.4	26.0	36620	3	US-09-952-060-30	Sequence 30, Appli
41	49.4	26.0	37474	3	US-09-952-060-25	Sequence 25, Appli
42	49.4	26.0	38519	3	US-09-952-060-28	Sequence 28, Appli
43	47.8	25.2	12445	3	US-09-865-022-2	Sequence 2, Appli
44	42	22.1	50	2	US-08-171-389-579	Sequence 579, App
45	42	22.1	50	2	US-08-171-389-580	Sequence 580, App

ALIGNMENTS

RESULT 1
US-08-333-706-1
; Sequence 1, Application US/08333706
; Patent No. 5612213
; GENERAL INFORMATION:
; APPLICANT: Chan, Shan-Yuen
; TITLE OF INVENTION: Vector and Mammalian Cell Line Having Improved
; TITLE OF INVENTION: Productivity
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: Fourth and Parker Streets
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/075,209
; FILING DATE: 10-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: CL-208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)420-5511
; TELEFAX: (510)428-4703
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-333-706-1

Query Match 26.0%; Score 49.4; DB 2; Length 382;
Best Local Similarity 83.6%; Pred. No. 1.5e-06;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:52:47 ; Search time 1231.06 Seconds
(without alignments)
7221.025 Million cell updates/sec

Title: US-10-781-055A-35

Perfect score: 190

Sequence: 1 aaatgacataggaactga.....ctctcagtcacgacgacaa 190

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_est1:*
2: gb_est2:*
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6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	19.5	1068	BM921844	BM921844 AGENCOURT
2	36.8	19.4	984	CZ386907	CZ386907 ZMMBF0163
3	36.4	19.2	549	CZ439879	CZ439879 OA_BBa009
4	35.6	18.7	846	DR408103	DR408103 mun20d02.
5	35.4	18.6	918	AG841160	AG841160 Oryza sat
6	34.8	18.3	608	DN871503	DN871503 nad13h05.
7	34.6	18.2	674	CE814538	CE814538 tigr-gss-
8	34.4	18.1	754	AO288311	AO288311 abxb0032L
9	34.4	18.1	1078	DR147979	DR147979 49078488
10	34.2	18.0	758	EG395886	EG395886 602458681
11	34.2	18.0	2225	BC033179	BC033179 Homo sapi
12	34	17.9	636	CL770232	CL770232 OR_BBa014
13	34	17.9	717	AO419418	AO419418 RCT-11-2
14	34	17.9	1302	BM456102	BM456102 AGENCOURT
15	34	17.9	1494	BQ059578	BQ059578 AGENCOURT
16	33.8	17.8	1149	CL5972671	CL5972671 OsIFCC023
17	33.6	17.7	333	BY150204	BY150204 BY150204
18	33.6	17.7	610	BI393079	BI393079 Pppln.pk0
19	33.6	17.7	643	BI390903	BI390903 Pppln.pk0
20	33.6	17.7	705	CZ426480	CZ426480 1022183 R
21	33.6	17.7	708	CZ406542	CZ406542 1002245 R
22	33.6	17.7	822	BU159228	BU159228 AGENCOURT

C	23	33.6	17.7	827	10	CZ353914	CZ353914 ZMMBF0091
	24	33.6	17.7	943	10	CZ399845	CZ399845 ZMMBF0181
	25	33.6	17.7	1113	3	BI872862	BI872862 603397470
	26	33.4	17.6	374	2	BE955554	BE955554 UI-M-CE1-
	27	33.4	17.6	779	3	BI601205	BI601205 603245717
	28	33.4	17.6	1112	8	DR737645	DR737645 EGAS08286
	29	33.2	17.5	289	2	BB870121	BB870121 BB870121
	30	33.2	17.5	606	8	DN436751	DN436751 LIB4217-0
	31	33.2	17.5	673	8	DN416974	DN416974 LIB4215-0
	32	33.2	17.5	1045	10	CL495014	CL495014 SAIL_604
	33	33	17.4	334	5	BY794202	BY794202 BY794202
	34	33	17.4	390	10	CE848591	CE848591 tigr-gss-
	35	33	17.4	458	7	CF853400	CF853400 pnc008xk
	36	33	17.4	615	7	BI382039	BI382039 BEIG2_000
	37	33	17.4	694	7	CK807009	CK807009 AGENCOURT
	38	33	17.4	1152	10	AG048286	AG048286 Pan trogl
	39	33	17.4	1378	3	BM807238	BM807238 AGENCOURT
	40	33	17.4	1664	10	AG082918	AG082918 Pan trogl
	41	32.8	17.3	490	8	CX802784	CX802784 JGI_CAAJ1
	42	32.8	17.3	582	3	BP303844	BP303844 BP303844
	43	32.8	17.3	621	2	BF673001	BF673001 602152887
	44	32.8	17.3	747	6	CA170582	CA170582 SCQSS8105
	45	32.8	17.3	948	2	BG397609	BG397609 602438652

ALIGNMENTS

RESULT 1
BM921844
LOCUS
DEFINITION
5', mRNA sequence.
AGENCOURT_6706906 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753443
BM921844
BM921844.1 GI:19372223
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1068)
NIH-MGC <http://mgc.mci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12789 row: d column: 20
High quality sequence stop: 270.
Location/Qualifiers
1..1068
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5753443"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code

FEATURES
source

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:41:05 ; Search time 172.221 Seconds
(without alignments)
7352.695 Million cell updates/sec

Title: US-10-781-055A-35

Perfect score: 190

Sequence: 1 aaatgacataggaactga.....ctctcagtcctcagcgatcaa 190

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
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8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190	100.0	190	13	ADR90242
2	190	100.0	596	13	ADR90244
3	190	100.0	614	13	ADR90243
4	49.4	26.0	382	2	AAQ79748
5	49.4	26.0	382	2	AAQ79748
6	49.4	26.0	382	2	AAQ79748
7	49.4	26.0	561	1	AAQ50287
8	49.4	26.0	578	1	AAQ50288
9	49.4	26.0	642	2	AAQ54210
10	49.4	26.0	642	2	AAQ58456
11	49.4	26.0	642	2	AAQ58456
12	49.4	26.0	642	2	AAQ58456
13	49.4	26.0	824	1	AAQ13632
14	49.4	26.0	848	2	AAQ13632
15	49.4	26.0	873	3	AAQ39104
16	49.4	26.0	874	1	AAQ70082
17	49.4	26.0	874	2	AAQ3825
18	49.4	26.0	874	2	AAQ54209
19	49.4	26.0	874	2	AAQ58455

20	49.4	26.0	874	2	AAQ36645
21	49.4	26.0	874	2	AAQ15955
22	49.4	26.0	874	2	AAQ43793
23	49.4	26.0	874	2	AAQ95171
24	49.4	26.0	874	2	AAQ18483
25	49.4	26.0	874	5	AAQ45120
26	49.4	26.0	3788	3	AAQ293330
27	49.4	26.0	3788	5	AAQ21318
28	49.4	26.0	5155	6	AAQ42468
29	49.4	26.0	5155	8	AAQ42468
30	49.4	26.0	5155	8	AAQ42468
31	49.4	26.0	5365	1	AAQ90646
32	49.4	26.0	5374	3	AAQ60706
33	49.4	26.0	5462	1	AAQ90649
34	49.4	26.0	5518	1	AAQ90647
35	49.4	26.0	5566	1	AAQ90648
36	49.4	26.0	6149	1	AAQ90645
37	49.4	26.0	6151	1	AAQ90644
38	49.4	26.0	6151	2	AAQ05608
39	49.4	26.0	6151	2	AAQ03006
40	49.4	26.0	6165	2	AAQ20324
41	49.4	26.0	7316	2	AAQ04555
42	49.4	26.0	7377	2	AAQ05607
43	49.4	26.0	7377	2	AAQ03005
44	49.4	26.0	7522	10	ACC71556
45	49.4	26.0	7711	6	ABK91497

ALIGNMENTS

RESULT 1

ADR90242

ID ADR90242 standard; DNA; 190 BP.

XX

AC ADR90242;

XX

DT 18-NOV-2004 (first entry)

XX

DE SP72 promoter DNA #1.

XX

Promoter/enhancer; cancer; infectious disease; inflammatory disease; tuberculosis; hepatitis B; HIV-1; influenza; malaria; cytostatic;

XX

OS Unidentified.

XX

PN US2004171573-A1.

XX

PD 02-SEP-2004.

XX

PP 18-FEB-2004; 2004US-00781055.

XX

PR 18-FEB-2003; 2003US-0448166P.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Johnston S, Qu B;

XX

DR WPI; 2004-634560/61.

XX

New nucleic acid segment comprises SP72 synthetic promoter/enhancer, useful as a vaccine for genetic immunization or for gene therapy for treating or preventing cancers, infectious diseases, or inflammatory diseases.

XX

Claim 12; SEQ ID NO 35; 34pp; English.

XX

The present invention provides nucleic acid segments comprising a synthetic promoter/enhancer or its complement. The invention is useful for treating or preventing diseases or conditions including cancers, infectious diseases and inflammatory diseases such as viral and parasitic including tuberculosis, hepatitis B, HIV-1, influenza and malaria. The

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OM nucleic - nucleic search, using sw model
Run on: March 28, 2006, 05:46:12 ; Search time 1034.96 Seconds
(without alignments)
10435.462 Million cell updates/sec

Title: US-10-781-055A-35
Perfect score: 190
Sequence: 1 aaatgacataggaactga.....ctctcagtcagcgatcaa 190

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 5883141 seqs, 28421725653 residues 11766282
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: gb_in:*
 - 3: gb_env:*
 - 4: gb_on:*
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 - 7: gb_ph:*
 - 8: gb_pi:*
 - 9: gb_ro:*
 - 10: gb_scs:*
 - 11: gb_sy:*
 - 12: gb_un:*
 - 13: gb_vi:*
 - 14: gb_htg:*
 - 15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	49.4	26.0	560	6	I02395 Sequence 1
3	49.4	26.0	578	6	I02396 Sequence 2
4	49.4	26.0	642	6	E01427 DNA sequenc
5	49.4	26.0	642	6	E59622 Human prote
6	49.4	26.0	642	6	I05120 Sequence 11
7	49.4	26.0	642	6	BD014699 Recombina
8	49.4	26.0	643	6	I71451 Sequence 21
9	49.4	26.0	872	6	I71450 Sequence 20
10	49.4	26.0	874	6	E01426 DNA sequenc
11	49.4	26.0	874	6	E59621 Human prote
12	49.4	26.0	874	6	I05111 Sequence 10
13	49.4	26.0	874	6	I07642 Sequence 11
14	49.4	26.0	874	6	AR365523 Sequence
15	49.4	26.0	874	6	BD014698 Recombina
16	49.4	26.0	2898	6	ARI78237 Sequence
17	49.4	26.0	3788	6	BD223711 Methylati
18	49.4	26.0	3788	6	AX282868 Sequence

19	49.4	26.0	5155	6	AR214348 Sequence
20	49.4	26.0	5155	6	AR654117 Sequence
21	49.4	26.0	5365	6	I09267 Sequence 34
22	49.4	26.0	5374	6	BD247396 Primer-as
23	49.4	26.0	5374	6	AR533276 Sequence
24	49.4	26.0	5413	6	I09270 Sequence 37
25	49.4	26.0	5462	6	BD247395 Primer-as
26	49.4	26.0	5462	6	AR533275 Sequence
27	49.4	26.0	5518	6	I09268 Sequence 35
28	49.4	26.0	5566	6	I09269 Sequence 36
29	49.4	26.0	6149	6	I09252 Sequence 19
30	49.4	26.0	6151	6	I09251 Sequence 18
31	49.4	26.0	7069	11	U02442 Cloning vec
32	49.4	26.0	7711	6	AX427811 Sequence
33	49.4	26.0	7789	6	AX427807 Sequence
34	49.4	26.0	7789	6	AX427810 Sequence
35	49.4	26.0	7792	6	AX427808 Sequence
36	49.4	26.0	7819	6	CS078969 Sequence
37	49.4	26.0	7828	6	AX427809 Sequence
38	49.4	26.0	7841	6	CS078964 Sequence
39	49.4	26.0	7844	6	CS078966 Sequence
40	49.4	26.0	7852	6	CS078967 Sequence
41	49.4	26.0	7867	6	AX427804 Sequence
42	49.4	26.0	7870	6	AX427801 Sequence
43	49.4	26.0	7870	6	AX427805 Sequence
44	49.4	26.0	7885	6	AX427806 Sequence
45	49.4	26.0	7906	6	AX427802 Sequence

ALIGNMENTS

RESULT 1
I36987 136987 382 bp DNA linear PAT 13-MAY-1997
LOCUS Sequence 1 from patent US 5612213.
ACCESSION I36987
VERSION I36987.1 GI:2084947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 382)
AUTHORS Chan, S. Y.
TITLE Method of selecting mammalian cell lines having improved productivity
JOURNAL Patent: US 5612213-A 1 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..382
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 26.0%; Score 49.4; DB 6; Length 382;
Best Local Similarity 83.6%; Pred. No. 0.013;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 82 CCGGTGTTCTCCTGAAGGGCGCCCTATATAAGGGGGGGCGCGCTTCGTCCTCATCTGGA 141
Db 197 CGGGTCTTCTCCTGAAGGGGGCGCTATAAAGGGGGTGGGGCGCGCTTCCTCTCTT 256
QY 142 CCGCGTC 148
Db 257 CCGCATC 263

RESULT 2
I02395 102395 560 bp ss-DNA linear PAT 18-MAY-1993
LOCUS Sequence 1 from Patent US 4510245.
DEFINITION I02395
ACCESSION I02395
VERSION I02395.1 GI:268039
KEYWORDS

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:24:40 ; Search time 738.614 Seconds
(without alignments)
3216.574 Million cell updates/sec

Title: US-10-781-055A-37
Perfect score: 596
Sequence: 1 csgtatcatgttctcgat.....ctctcagtcagcgatcaa 596

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9258654 seqs, 1993127192 residues

Total number of hits satisfying chosen parameters: 18517308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New.*

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- 2: /SIDSS/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 9: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 10: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 11: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 14: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 15: /SIDSS/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	8.3	5155	14	US-11-005-216-3
2	49.4	8.3	33014	14	US-11-077-716-1
3	49.4	8.3	33592	11	US-11-249-873-1
4	49.4	8.3	33699	11	US-11-249-873-3
5	49.4	8.3	33988	11	US-11-249-873-14
6	49.4	8.3	34341	11	US-11-249-873-2
7	49.4	8.3	34448	11	US-11-249-873-4
8	49.4	8.3	34555	8	US-10-623-155-479
9	49.4	8.3	34737	11	US-11-249-873-15
10	49.4	8.3	35696	8	US-10-860-436-1
11	49.4	8.3	35724	11	US-11-249-873-13
12	49.4	8.3	35893	8	US-10-860-436-2
13	49.4	8.3	35935	14	US-11-127-832-4
14	49.4	8.3	35935	14	US-11-127-832-5
15	49.4	8.3	35937	14	US-11-127-832-3
16	49.4	8.3	36114	11	US-11-249-873-16
17	47.8	8.0	12445	9	US-10-948-344-2
18	37.4	6.3	1815	9	US-10-932-182A-76020

19	37.4	6.3	1815	9	US-10-932-182A-76020	Sequence 76020, A
20	36.6	6.1	794	10	US-10-301-480-577081	Sequence 577081, A
21	36.6	6.1	794	10	US-10-301-480-1190490	Sequence 1190490, A
C 22	36.2	6.1	606	6	US-09-925-065A-435628	Sequence 435628, A
C 23	36.2	6.1	634	10	US-10-301-480-497505	Sequence 497505, A
C 24	36.2	6.1	634	10	US-10-301-480-1110914	Sequence 1110914, A
C 25	36.2	6.1	635	10	US-10-301-480-497506	Sequence 497506, A
C 26	36.2	6.1	635	10	US-10-301-480-1110915	Sequence 1110915, A
C 27	36.2	6.1	647	6	US-09-925-065A-435629	Sequence 435629, A
C 28	35	5.9	35100	14	US-11-127-832-26	Sequence 26, Appl
C 29	34.8	5.8	536	6	US-09-925-065A-122252	Sequence 122252, A
C 30	34.8	5.8	536	6	US-09-925-065A-122253	Sequence 122253, A
C 31	34.4	5.8	536	6	US-09-925-065A-122254	Sequence 122254, A
C 32	34.4	5.8	564	6	US-09-925-065A-635665	Sequence 635665, A
C 33	34.2	5.7	191684	14	US-11-121-086-2	Sequence 2, Appl
C 34	33.8	5.7	645179	8	US-10-995-561-13293	Sequence 13293, A
C 35	33.6	5.6	681	8	US-10-750-185-63747	Sequence 63747, A
C 36	33.6	5.6	681	8	US-10-750-623-63747	Sequence 63747, A
C 37	33.4	5.6	624	6	US-09-925-065A-544994	Sequence 544994, A
C 38	33.4	5.6	4436	14	US-11-122-329-117	Sequence 117, App
C 39	33	5.5	624	6	US-09-925-065A-544993	Sequence 544993, A
C 40	33	5.5	624	10	US-10-301-480-335191	Sequence 335191, A
C 41	33	5.5	624	10	US-10-301-480-948600	Sequence 948600, A
C 42	33	5.5	625	6	US-09-925-065A-256474	Sequence 256474, A
C 43	33	5.5	825	6	US-09-925-065A-37189	Sequence 37189, A
C 44	33	5.5	825	9	US-10-301-480-138427	Sequence 138427, A
C 45	33	5.5	825	10	US-10-301-480-751836	Sequence 751836, A

ALIGNMENTS

RESULT 1

US-11-005-216-3
; Sequence 3, Application US/11005216
; Publication No. US20050287633A1
; GENERAL INFORMATION:
; APPLICANT: McIntyre, Peter
; APPLICANT: James, Iain Fraser
; TITLE OF INVENTION: Human Vanilloid Receptor
; FILE REFERENCE: 4-30875A
; CURRENT APPLICATION NUMBER: US/11/005,216
; CURRENT FILING DATE: 2004-12-06
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US/09/533,220
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9907097.1
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 1.30
; SEQ ID NO 3
; LENGTH: 5155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-005-216-3

Query Match 8.3%; Score 49.4; DB 14; Length 5155;
Best Local Similarity 83.6%; Pred. No. 0.00033;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 488 CCGGTGTTCTGAAGGGCGCTATATAAGGGGGGGCGGTCGTCCTCATCTGGA 547
Db 567 CCGGTGTTCTGAAGGGCGCTATATAAGGGGGGGCGGTCGTCCTCATCTCTT 626
QY 548 CCGCGTC 554
Db 627 CCGCATC 633

RESULT 2

US-11-077-716-1
; Sequence 1, Application US/11077716
; Publication No. US20050260180A1
; GENERAL INFORMATION:

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:20:15 ; Search time 777.354 Seconds
(without alignments)
6340.158 Million cell updates/sec

Title: US-10-781-055A-37

Perfect score: 596

Sequence: 1 CGGTACATGATGTTCTCGAT.....CTCTCAGTCTCAGCATCAA 596

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main.*

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- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	596	7	US-10-781-055-37
2	568	95.3	614	7	US-10-781-055-36
3	190	31.9	190	7	US-10-781-055-35
4	60	10.1	60	7	US-10-781-055-3
5	51	8.6	51	7	US-10-781-055-1
6	49.4	8.3	3788	3	US-09-392-462-1
7	49.4	8.3	3788	3	US-09-540-991-1
8	49.4	8.3	3788	6	US-10-291-041-1
9	49.4	8.3	3788	7	US-10-351-603-1
10	49.4	8.3	5155	5	US-10-128-853-3
11	49.4	8.3	5374	5	US-10-007-357-7
12	49.4	8.3	5462	5	US-10-007-357-6
13	49.4	8.3	7522	8	US-10-491-121-36
14	49.4	8.3	7711	7	US-10-359-120-49
15	49.4	8.3	7711	8	US-10-491-121-35
16	49.4	8.3	7789	7	US-10-359-120-45
17	49.4	8.3	7789	7	US-10-359-120-48
18	49.4	8.3	7792	7	US-10-359-120-46
19	49.4	8.3	7828	7	US-10-359-120-47
20	49.4	8.3	7828	7	US-10-359-120-42
21	49.4	8.3	7870	7	US-10-359-120-39
22	49.4	8.3	7870	7	US-10-359-120-43
23	49.4	8.3	7885	7	US-10-359-120-44

24	49.4	8.3	7906	7	US-10-359-120-40
25	49.4	8.3	7909	7	US-10-359-120-41
26	49.4	8.3	7948	7	US-10-359-120-36
27	49.4	8.3	7963	7	US-10-359-120-37
28	49.4	8.3	7966	7	US-10-359-120-38
29	49.4	8.3	7987	7	US-10-359-120-35
30	49.4	8.3	8131	8	US-10-491-121-12
31	49.4	8.3	8146	8	US-10-491-121-20
32	49.4	8.3	8199	8	US-10-491-121-29
33	49.4	8.3	8221	8	US-10-491-121-27
34	49.4	8.3	8238	3	US-09-482-682-50
35	49.4	8.3	8256	8	US-10-491-121-32
36	49.4	8.3	8338	8	US-10-491-121-26
37	49.4	8.3	8439	8	US-10-491-121-28
38	49.4	8.3	10783	8	US-10-491-121-25
39	49.4	8.3	30365	7	US-10-384-136-4
40	49.4	8.3	31183	7	US-10-431-598-19
41	49.4	8.3	31183	8	US-10-825-282-4
42	49.4	8.3	31672	7	US-10-384-136-3
43	49.4	8.3	31880	7	US-10-427-717-507
44	49.4	8.3	31976	8	US-10-766-307A-1
45	49.4	8.3	31976	8	US-10-766-307A-2

ALIGNMENTS

RESULT 1

US-10-781-055-37
; Sequence 37, Application US/10781055
; Publication No. US20040171573A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN
; APPLICANT: QU, BAO-XI
; TITLE OF INVENTION: RATIONALLY DESIGNED AND CHEMICALLY SYNTHESIZED
; FILE REFERENCE: PROMOTER FOR GENETIC VACCINE AND GENE THERAPY
; CURRENT APPLICATION NUMBER: US/10/781,055
; CURRENT FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/448,166
; PRIOR FILING DATE: 2003-02-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-781-055-37

Query Match 100.0%; Score 596; DB 7; Length 596;
Best Local Similarity 100.0%; Pred. No. 7.3e-186;
Matches 596; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGGTACATGATGTTCTCGATGCAATATCACTGTAAGTCAAAAATAGGTCAATCAATAA 60
Db	1	CGGTACATGATGTTCTCGATGCAATATCACTGTAAGTCAAAAATAGGTCAATCAATAA 60
QY	61	GAGTGTAGGACGGAGAGGGGGAACAGAACAGACAGTCTGACGTGACGAGCAGT 120
Db	61	GAGTGTAGGACGGAGAGGGGGAACAGAACAGACAGTCTGACGTGACGAGCAGT 120
QY	121	TGCCCTTTGAAACGTTAAACGTTTACGTTGAGTCTGAGTCTGATTAATTAATTA 180
Db	121	TGCCCTTTGAAACGTTAAACGTTTACGTTGAGTCTGAGTCTGATTAATTAATTA 180
QY	181	GCCAAAGGGCCAAAGGCAACGTTTATGCAAAATGCAAAATGAGAACAGGGGGGGG 240
Db	181	GCCAAAGGGCCAAAGGCAACGTTTATGCAAAATGCAAAATGAGAACAGGGGGGGG 240
QY	241	CGGACATCGTTCACAGTTTCTGTTTCAATTTCTTCTTCTTCTTCTTCTTCTTCTT 300

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 06:03:35 ; Search time 159.217 Seconds
(without alignments)
6653.974 Million cell updates/sec

Title: US-10-781-055A-37

Perfect score: 596

Sequence: 1 cgggtacagatgttcgat.....ctctcagtcagcagatcaa 596

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/PCUS COMB.seq:*
- 7: /cgn2_6/prodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49.4	8.3	382	2	US-08-333-706-1
2	49.4	8.3	643	2	US-08-458-372-21
3	49.4	8.3	643	8	US-09-384-327-21
4	49.4	8.3	872	2	US-08-458-372-20
5	49.4	8.3	872	8	US-09-384-327-20
6	49.4	8.3	874	9	5506118-10
7	49.4	8.3	2898	3	US-09-051-696-7
8	49.4	8.3	5155	3	US-09-533-220A-3
9	49.4	8.3	5155	3	US-10-128-853-3
10	49.4	8.3	5374	3	US-10-007-357-7
11	49.4	8.3	5462	3	US-10-007-357-6
12	49.4	8.3	6151	6	PCT-US91-02954-12
13	49.4	8.3	6306	6	PCT-US94-00658-1
14	49.4	8.3	32166	3	US-09-562-930-11
15	49.4	8.3	32798	3	US-09-604-6948-1
16	49.4	8.3	34303	2	US-08-735-609-4
17	49.4	8.3	34303	2	US-08-735-609-4
18	49.4	8.3	34303	3	US-09-315-372-4
19	49.4	8.3	34303	3	US-09-244-752-4
20	49.4	8.3	34303	3	US-09-245-497-4
21	49.4	8.3	34303	3	US-09-562-919-4
22	49.4	8.3	34382	2	US-08-374-483-6
23	49.4	8.3	34427	3	US-09-111-911-5
24	49.4	8.3	35408	3	US-08-973-334-3

25	49.4	8.3	35408	3	US-09-563-869A-3	Sequence 3, Appli
26	49.4	8.3	35408	3	US-08-549-489-3	Sequence 3, Appli
27	49.4	8.3	35871	3	US-09-956-335-2	Sequence 2, Appli
28	49.4	8.3	35935	2	US-08-735-609-1	Sequence 1, Appli
29	49.4	8.3	35935	2	US-08-735-609-1	Sequence 1, Appli
30	49.4	8.3	35935	3	US-08-379-452-43	Sequence 43, Appli
31	49.4	8.3	35935	3	US-09-315-372-1	Sequence 1, Appli
32	49.4	8.3	35935	3	US-09-244-752-1	Sequence 1, Appli
33	49.4	8.3	35935	3	US-09-405-670-43	Sequence 43, Appli
34	49.4	8.3	35935	3	US-09-245-497-1	Sequence 1, Appli
35	49.4	8.3	35935	3	US-09-562-919-1	Sequence 1, Appli
36	49.4	8.3	35935	3	US-09-782-378A-4	Sequence 4, Appli
37	49.4	8.3	35935	3	US-09-782-378A-5	Sequence 5, Appli
38	49.4	8.3	35937	3	US-09-782-378A-3	Sequence 3, Appli
39	49.4	8.3	35978	3	US-09-956-335-1	Sequence 1, Appli
40	49.4	8.3	36620	3	US-09-952-060-30	Sequence 30, Appli
41	49.4	8.3	37474	3	US-09-952-060-25	Sequence 25, Appli
42	49.4	8.3	38519	3	US-09-952-060-28	Sequence 28, Appli
43	47.8	8.0	12445	3	US-09-865-022-2	Sequence 2, Appli
c	44.8	7.5	7218	2	US-08-232-463-14	Sequence 14, Appli
45	42	7.0	50	2	US-08-171-389-579	Sequence 579, App

ALIGNMENTS

RESULT 1
US-08-333-706-1
; Sequence 1, Application US/08333706
; Patent No. 5612213
; GENERAL INFORMATION:
; APPLICANT: Chan, Sham-Yuen
; TITLE OF INVENTION: Vector and Mammalian Cell Line Having Improved
; TITLE OF INVENTION: Productivity
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: Fourth and Parker Streets
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,706
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/075,209
; FILING DATE: 10-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Giblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: CL-208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)420-5511
; TELEFAX: (510)428-4703
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 382
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-333-706-1

Query Match 8.3%; Score 49.4; DB 2; Length 382;
Best Local Similarity 83.6%; Fred. No. 9.6e-06;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:52:47 ; Search time 3861.65 Seconds
(without alignments)
7221.025 Million cell updates/sec

Title: US-10-781-055A-37
Perfect score: 596
Sequence: 1 cggatcatgtgtcttcgat.....ctctcagttctcagcgtacaa 596

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs; 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	47.6	8.0	1151	10	CL048546 CH216-68C
C 2	39.6	6.6	1201	10	AL106532 Drosophila
C 3	38.8	6.5	859	10	AL055406 Drosophila
C 4	38.2	6.4	1068	3	BM921844 AGENCOURT
C 5	38	6.4	409	1	AI857142 MENAd-A1
C 6	37.4	6.3	796	7	CR412210 CH412210
C 7	37.2	6.2	1079	9	CC230752 CH216-114
C 8	36.8	6.2	568	6	CD125835 MF1-0001U
C 9	36.8	6.2	584	10	CZ386907 ZMMBF0163
C 10	36.8	6.2	997	10	CNS005TE
C 11	36.6	6.1	794	8	DN112025 1111185 M
C 12	36.4	6.1	549	10	C2439879
C 13	36.4	6.1	821	5	BX731308 BX731308
C 14	36.4	6.1	1064	9	BZ247726
C 15	36.4	6.1	1200	6	CD503874
C 16	36.2	6.1	655	10	CE451080
C 17	36.2	6.1	914	1	AL544144
C 18	36	6.0	612	9	BH679464
C 19	36	6.0	737	8	DR399051
C 20	36	6.0	1030	10	CNS02082
C 21	35.6	6.0	589	10	CE343398
C 22	35.6	6.0	846	8	DR408103

23	35.6	6.0	1078	6	CF223929
24	35.4	5.9	360	5	C61810
25	35.4	5.9	444	9	AQ767046
26	35.4	5.9	737	10	AG436603
27	35.4	5.9	817	10	CZ998292
28	35.4	5.9	856	11	CNS035DM
29	35.4	5.9	918	10	AG841160
30	35.4	5.9	1113	8	DN667583
31	35.4	5.9	1201	5	EX377655
32	35.2	5.9	677	9	BZ412845
33	35.2	5.9	747	7	CO393315
34	35.2	5.9	831	6	CB558496
35	35	5.9	451	3	BJ898349
36	35	5.9	710	2	BE034031
37	35	5.9	840	9	AZ212232
38	35	5.9	884	10	CZ209683
39	35	5.9	1014	10	CL109372
40	35	5.9	1112	8	DR737645
41	34.8	5.8	227	8	M79041
42	34.8	5.8	339	8	M79042
43	34.8	5.8	415	9	AQ755672
44	34.8	5.8	608	8	DN871503
45	34.8	5.8	698	8	CV850179

ALIGNMENTS

RESULT 1
CL048546/c
LOCUS
DEFINITION
CH216-68C22_RM1.1 CH216 Xenopus tropicalis genomic clone
CH216-68C22, genomic survey sequence.
CL048546
GSS.
CL048546.1 GI:40504459
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE
1 (bases 1 to 1151)
Krenitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E., and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGAGA
Class: BAC ends
High quality sequence start: 25
High quality sequence stop: 438.
FEATURES
source
1..1151
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-68C22"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pFARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN

Query Match 8.0%; Score 47.6; DB 10; Length 1151;
Best Local Similarity 50.9%; Pred No. 0.0068;
Matches 113; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:41:05 ; Search time 540.231 Seconds
(without alignments)
7352.695 Million cell updates/sec

Title: US-10-781-055A-37
Perfect score: 596
Sequence: 1 cggatcatgtgtctctgat.....ctctcagtcacgcatcaa 596

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseqn_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	596	13	ADR90244
2	568	95.3	614	13	ADR90243
3	190	31.9	190	13	ADR90242
4	60	10.1	60	13	ADR90218
5	51	8.6	51	13	ADR90216
6	49.4	8.3	382	2	AAQ79748
7	49.4	8.3	382	2	AAQ79748
8	49.4	8.3	382	2	AAQ79748
9	49.4	8.3	382	2	AAQ79748
10	49.4	8.3	382	2	AAQ79748
11	49.4	8.3	382	2	AAQ79748
12	49.4	8.3	382	2	AAQ79748
13	49.4	8.3	382	2	AAQ79748
14	49.4	8.3	382	2	AAQ79748
15	49.4	8.3	382	2	AAQ79748
16	49.4	8.3	382	2	AAQ79748
17	49.4	8.3	382	2	AAQ79748
18	49.4	8.3	382	2	AAQ79748
19	49.4	8.3	382	2	AAQ79748

20	49.4	8.3	874	2	AAQ54209
21	49.4	8.3	874	2	AAQ58455
22	49.4	8.3	874	2	AAQ58455
23	49.4	8.3	874	2	AAQ58455
24	49.4	8.3	874	2	AAQ58455
25	49.4	8.3	874	2	AAQ58455
26	49.4	8.3	874	2	AAQ58455
27	49.4	8.3	874	2	AAQ58455
28	49.4	8.3	874	2	AAQ58455
29	49.4	8.3	874	2	AAQ58455
30	49.4	8.3	874	2	AAQ58455
31	49.4	8.3	874	2	AAQ58455
32	49.4	8.3	874	2	AAQ58455
33	49.4	8.3	874	2	AAQ58455
34	49.4	8.3	874	2	AAQ58455
35	49.4	8.3	874	2	AAQ58455
36	49.4	8.3	874	2	AAQ58455
37	49.4	8.3	874	2	AAQ58455
38	49.4	8.3	874	2	AAQ58455
39	49.4	8.3	874	2	AAQ58455
40	49.4	8.3	874	2	AAQ58455
41	49.4	8.3	874	2	AAQ58455
42	49.4	8.3	874	2	AAQ58455
43	49.4	8.3	874	2	AAQ58455
44	49.4	8.3	874	2	AAQ58455
45	49.4	8.3	874	2	AAQ58455

ALIGNMENTS

RESULT 1

ADR90244

ID ADR90244 standard; DNA; 596 BP.

AC ADR90244;

DT 18-NOV-2004 (first entry)

DE SP72 promoter DNA #3.

XX Promoter/enhancer; cancer; infectious disease; inflammatory disease;

XX tuberculosis; hepatitis B; HIV-1; influenza; malaria; cytostatic;

XX vaccine; gene therapy; SP72 promoter; ds.

XX Unidentified.

XX US2004171573-A1.

XX 02-SEP-2004.

XX 18-FEB-2004; 2004US-00781055.

XX 18-FEB-2003; 2003US-0448166P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Johnston S, Qu B;

XX WPI; 2004-634560/61.

XX New nucleic acid segment comprises SP72 synthetic promoter/enhancer,

XX useful as a vaccine for genetic immunization or for gene therapy for

XX treating or preventing cancers, infectious diseases, or inflammatory

XX diseases.

XX Claim 14; SEQ ID NO 37; 34pp; English.

XX The present invention provides nucleic acid segments comprising a

XX synthetic promoter/enhancer or its complement. The invention is useful

XX for treating or preventing diseases or conditions including cancers,

XX infectious diseases and inflammatory diseases such as viral and parasitic

XX including tuberculosis, hepatitis B, HIV-1, influenza and malaria. The

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OM nucleic - nucleic search, using sw model

Run on: March 28, 2006, 05:46:12 ; Search time 3246.5 Seconds
(without alignments)
10435.462 Million cell updates/sec

Title: US-10-781-055A-37

Perfect score: 596

Sequence: 1 cggatcatgatgtcttcgat.....ctctcagtcgcgatcaa 596

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 588141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sta.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49.4	8.3	382	6 I36987	I36987 Sequence 1
2	49.4	8.3	560	6 I02395	I02395 Sequence 1
3	49.4	8.3	578	6 I02396	I02396 Sequence 2
4	49.4	8.3	642	6 E01427	E01427 DNA sequenc
5	49.4	8.3	642	6 E59622	E59622 Human prote
6	49.4	8.3	642	6 I05120	I05120 Sequence 11
7	49.4	8.3	642	6 BD014699	BD014699 Recombina
8	49.4	8.3	643	6 I71451	I71451 Sequence 21
9	49.4	8.3	872	6 I71450	I71450 Sequence 20
10	49.4	8.3	874	6 E01426	E01426 DNA sequenc
11	49.4	8.3	874	6 E59621	E59621 Human prote
12	49.4	8.3	874	6 I05111	I05111 Sequence 10
13	49.4	8.3	874	6 I07642	I07642 Sequence 11
14	49.4	8.3	874	6 AR365523	AR365523 Sequence
15	49.4	8.3	874	6 BD014698	BD014698 Recombina
16	49.4	8.3	2898	6 ARI178237	ARI178237 Sequence
17	49.4	8.3	3788	6 BD223711	BD223711 Methylati
18	49.4	8.3	3788	6 AX282868	AX282868 Sequence

19	49.4	8.3	5155	6 AR214348	AR214348 Sequence
20	49.4	8.3	5155	6 AR654117	AR654117 Sequence
21	49.4	8.3	5365	6 I09267	I09267 Sequence 34
22	49.4	8.3	5374	6 BD247396	BD247396 Primer-as
23	49.4	8.3	5374	6 AR533276	AR533276 Sequence 37
24	49.4	8.3	5413	6 I09270	I09270 Sequence 37
25	49.4	8.3	5462	6 BD247395	BD247395 Primer-as
26	49.4	8.3	5518	6 AR533275	AR533275 Sequence 35
27	49.4	8.3	5518	6 I09268	I09268 Sequence 35
28	49.4	8.3	5566	6 I09269	I09269 Sequence 36
29	49.4	8.3	6149	6 I09252	I09252 Sequence 19
30	49.4	8.3	6151	6 I09251	I09251 Sequence 18
31	49.4	8.3	7069	11 U02442	U02442 Cloning vec
32	49.4	8.3	7711	6 AX427811	AX427811 Sequence
33	49.4	8.3	7789	6 AX427807	AX427807 Sequence
34	49.4	8.3	7789	6 AX427810	AX427810 Sequence
35	49.4	8.3	7792	6 AX427808	AX427808 Sequence
36	49.4	8.3	7819	6 CS078969	CS078969 Sequence
37	49.4	8.3	7828	6 AX427809	AX427809 Sequence
38	49.4	8.3	7841	6 CS078964	CS078964 Sequence
39	49.4	8.3	7844	6 CS078966	CS078966 Sequence
40	49.4	8.3	7852	6 CS078967	CS078967 Sequence
41	49.4	8.3	7867	6 AX427804	AX427804 Sequence
42	49.4	8.3	7870	6 AX427801	AX427801 Sequence
43	49.4	8.3	7870	6 AX427805	AX427805 Sequence
44	49.4	8.3	7885	6 AX427806	AX427806 Sequence
45	49.4	8.3	7906	6 AX427802	AX427802 Sequence

ALIGNMENTS

RESULT 1
I36987
LOCUS I36987 382 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5612213.
ACCESSION I36987
VERSION I36987.1 GI:2084947
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 382)
AUTHORS Chaf,S.Y.
TITLE Method of selecting mammalian cell lines having improved productivity
JOURNAL Patent: US 5612213-A 1 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..382
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 8.3%; Score 49.4; DB 6; Length 382;
Best Local Similarity 83.6%; Pred. No. 0.0012;
Matches 56; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 488 CGGCTGTTCTCGAAGCGCGCTATATAGGGGGGGCGGCTTCCTCATCTCGA 547
Db 197 CGGCTGTTCTCGAAGCGCGCTATATAGGGGGGGCGGCTTCCTCATCTCTT 256
QY 548 CGCGGTC 554
Db 257 CGGCATC 263
RESULT 2
I02395
LOCUS I02395 560 bp ss-DNA linear PAT 18-MAY-1993
DEFINITION Sequence 1 from Patent US 4510245.
ACCESSION I02395
VERSION I02395.1 GI:268039
KEYWORDS